

Application No.: 09/742,684

Attorney Docket No.: SALK1720-6

Filing Date: December 19, 2000

(088802-3109)

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Amendments to the Claims

Please amend claim 11, and add new claims 18-36 as follows. Please cancel claims 12 and 13 without prejudice.

Listing of Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

1-10. (Cancelled).

11. (Currently amended) A method for screening a collection of compounds to determine those compounds which bind to receptors of the activin/TGF- β superfamily, said method comprising employing a vertebrate activin receptor in a competitive binding assay, wherein said vertebrate activin receptor is a novel receptor protein encoded by a nucleotide sequence which is:

(a) the nucleotide sequence of a cDNA molecule present in a vertebrate library, wherein the noncoding strand of the cDNA molecule hybridizes under conditions of low stringency with a probe comprising the contiguous sequence of nucleotides 128-1609 of SEQ ID NO:15; or

(b) a sequence degenerate with the sequence of a cDNA molecule according to (a);

wherein the receptor is further characterized by having the following domains, reading from the N-terminal end of said protein:

an extracellular, ligand-binding domain,
a hydrophobic, trans-membrane domain, and
an intracellular serine/threonine kinase domain, receptor domain having serine kinase-like activity.

12-17. (Cancelled).

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18. (New) A method according to claim 11, wherein said receptor is encoded by nucleotides having at least 70% sequence identity with respect to the contiguous nucleotide sequence of nucleotides 128-1609 of SEQ ID NO:15.

19. (New) A method according to claim 11, wherein said receptor is encoded by nucleotides having at least 80% sequence identity with respect to the contiguous nucleotide sequence of nucleotides 128-1609 of SEQ ID NO:15.

20. (New) A method according to claim 11, wherein said receptor is encoded by nucleotides having at least 90% sequence identity with respect to the contiguous nucleotide sequence of nucleotides 128-1609 of SEQ ID NO:15.

21. (New) A method according to claim 11, wherein the contiguous nucleotide sequence further comprises nucleotides 71-127 of SEQ ID NO:15.

22. (New) A method according to claim 18, wherein the contiguous nucleotide sequence further comprises nucleotides 71-127 of SEQ ID NO:15.

23. (New) A method according to claim 19, wherein the contiguous nucleotide sequence further comprises nucleotides 71-127 of SEQ ID NO:15.

24. (New) A method according to claim 20, wherein the contiguous nucleotide sequence further comprises nucleotides 71-127 of SEQ ID NO:15.

25. (New) A method according to claim 11, wherein said receptor comprises the amino acid sequence of residues 20-513 as set forth in SEQ ID NO:16.

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26. (New) A method according to claim 25, wherein said receptor further comprises the amino acid sequence of residues 1-19 as set forth in SEQ ID NO:16.

27. (New) A method for screening a collection of compounds to determine those compounds which bind to receptors of the activin/TGF- β superfamily, said method comprising employing a soluble polypeptide in a competitive binding assay,

wherein said soluble polypeptide is encoded by a nucleotide sequence which is:

(a) the nucleotide sequence of a cDNA molecule present in a vertebrate library, wherein the noncoding strand of the cDNA molecule hybridizes under conditions of low stringency with a probe comprising the contiguous sequence of nucleotides 128-472 of SEQ ID NO: 15; or
(b) a sequence degenerate with the sequence of a cDNA molecule according to (a).

28. (New) A method according to claim 27, wherein said polypeptide is encoded by nucleotides having at least 70% sequence identity with respect to the contiguous nucleotide sequence of nucleotides 128-472 of SEQ ID NO:15.

29. (New) A method according to claim 27, wherein said receptor is encoded by nucleotides having at least 80% sequence identity with respect to the contiguous nucleotide sequence of nucleotides 128-472 of SEQ ID NO:15.

30. (New) A method according to claim 27, wherein said receptor is encoded by nucleotides having at least 90% sequence identity with respect to the contiguous nucleotide sequence of nucleotides 128-472 of SEQ ID NO:15.

31. (New) A method according to claim 27, wherein the contiguous nucleotide sequence further comprises nucleotides 71-127 of SEQ ID NO:15.

32. (New) A method according to claim 28, wherein the contiguous nucleotide sequence further comprises nucleotides 71-127 of SEQ ID NO:15.

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33. (New) A method according to claim 29, wherein the contiguous nucleotide sequence further comprises nucleotides 71-127 of SEQ ID NO:15.

34. (New) A method according to claim 30, wherein the contiguous nucleotide sequence further comprises nucleotides 71-127 of SEQ ID NO:15.

35. (New) A method according to claim 27, wherein said receptor comprises the amino acid sequence of residues 20-134 as set forth in SEQ ID NO:16.

36. (New) A method according to claim 35, wherein said receptor further comprises the amino acid sequence of residues 1-19 as set forth in SEQ ID NO:16.